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CONTENTS/SUMMARIES

Summary: Homologous recombination is a ubiquitous biological process in which chromosomes pair, break, and rejoin by the sequential action of enzymes. Knowledge of the molecular mechanisms of this process is most extensive in procaryotes. This knowledge has guided the successful search for recombination-promoting enzymes in eucaryotes. Enzymatic studies on procaryotes have also provided the basis for detailed molecular models of recombination. Parallel genetic studies on recombination-deficient procaryotic mutants have led to the concept of alternative enzymatic pathways leading to recombination. Since the forms of deoxyribonucleic acid that recombine vary from circular duplexes to linear single strands, the pathways promoting recombination necessarily vary. This review discusses the forms of deoxyribonucleic acid that recombine following conjugation, transduction, transformation, and phage infection and during growth of partially diploid cells. The abilities of recombination-promoting enzymes to act on these deoxyribonucleic acid substrates are considered within the context of alternative recombinational pathways. Two molecular models of recombination that attempt to unify the genetic and enzymatic functions promoting recombination in these diverse circumstances are described.

Summary: Dictyostelium discoideum is an organism that has made the transition from single cells to a multicellular tissue of cooperating cells. The process of cellular aggregation by which the shift occurs is one of the better understood eucaryotic developmental progressions. This review describes aggregation and the biological and genetic means available to study it. A summary of known mutants and their phenotypes has been provided. Some mutant phenotypes have been given a biochemical basis which draws from the characterization of the macromolecules which mediate aggregation toward sources of cyclic adenosine 3',5'-phosphate (cAMP). The number of genes required for aggregation is likely to be small, and therefore there is good justification for inventing selection techniques to recover informative mutants which affect crucial steps in aggregation. The experimental arsenal of mutants and a parasexual genetic system to analyze them have been supplemented by selectable transformation vectors and the potential of integration of transformed sequences by homologous recombination. One of the effects of cAMP binding to cell surface receptors is to initiate chemotaxis, but that is not the only function of the cAMP receptor. The cells link the receptor to second messenger cascades used to control the expression of genes required

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for development. Conditions which stop chemotaxis by causing receptor adaptation also stop developmental gene expression, thus achieving a coordination of morphological and transcriptive events. Certain genes are exempt and continue to be transcribed. A model to explain the varieties of gene regulation elicited by pulses or constant amounts of extracellular cAMP is presented and genetic ways to proceed are suggested.

Summary: The physiological diversity of the purple nonsulfur photosynthetic bacteria has provided us with a unique opportunity to understand the complex interrelationships between gene control of various cellular synthetic pathways and the structural and functional parameters associated with photosynthesis. In particular, the synthesis of the photosynthetic membranes has been extensively studied in the bacterium Rhodobacter sphaeroides. This photosynthetic membrane is inducible by low oxygen tension and is further regulated by incident light intensity. Although the molecular regulatory mechanisms that control these activities are not fully understood, recent developments, summarized in this review, have elucidated the genetic and transcriptional organization for several components associated with photosynthetic membrane synthesis, assembly, structure, and function. Ongoing structural analysis of individual pigment-protein complexes purified from the photosynthetic membrane are discussed in terms of our ability to probe structure-function relationships of these specialized membrane complexes and the reactions that convert light energy to cellular energy. Analysis of the composition and assembly of photosynthetic membranes at the transcriptional and posttranscriptional levels in both steady-state cells and cells undergoing changes in physiological growth conditions have shed light on the regulation of the synthesis of pigment-protein complexes in the photosynthetic membrane and how synthesis and orientation of individual complexes are related to photosynthetic membrane assembly. The diversity of approaches used to analyze the structure and assembly of the photosynthetic membranes in the purple nonsulfur bacteria, such as R. sphaeroides, are discussed and have provided us with the most detailed molecular/genetic analysis of any biological membrane system.

Summary: The relative ease with which genetic and molecular manipulations can be carried out in the yeast Saccharomyces cerevisiae makes this organism extremely attractive as a model for investigating the molecular biology of deoxyribonucleic acid (DNA) repair in eucaryotic cells. Genetic analyses indicate that a surprisingly large number of gene functions are involved in cellular responses to genomic result. These genes have been organized into three largely nonoverlapping epistasis groups which probably reflect fundamentally discrete cellular responses to DNA damage. These include excision repair, recombinational repair, and repair associated with increased levels of mutagenesis. In recent years genes from each of the three epistasis groups have been isolated by molecular cloning, and their detailed characterization, sequencing, and overexpression have provided new insights into the molecular biology and biochemistry of various DNA repair modes in yeasts. This review traces the development of our current understanding of the complex genetics and cellular biology of DNA repair in S. cerevisiae and explores in detail the information obtained thus far from the study of isolated genes and the proteins they express.

Summary: The first thionucleoside in transfer ribonucleic acid (RNA), 4-thiouridine, was discovered in 1965. Since then, 10 sulfur-containing nucleosides have been isolated

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and identified in transfer RNA from various sources. Their structures, ultraviolet spectra, R_f values in several solvent systems, and electrophoretic mobilities at pH 3.5 are presented. Thionucleosides are not found in all organisms, and when they do occur they are restricted to certain locations in specific tRNAs. All 2-thiouridine derivatives occur at the first position of the anticodon. Normally, the oxygen atom at the 2-position of the uridine forms a hydrogen bond with the "wobble" bases U and G. When sulfur replaces this oxygen, the hydrogen bond between U and G is weak and hence tRNAs that contain 2-thiouridine derivatives do not bind to both the normal and wobble codons with the same efficiency. This can lead to differential rates of translation of messenger RNAs and consequent control of cellular function. Adenosine derivatives containing a methylthio group occur as the first nucleoside adjacent to the 3' end of the anticodon. Among these, the cytokinin-active nucleosides have been found in tRNAs whose codons start with U. Being adjacent to the anticodon, these nucleosides also influence the rate of translation. Both the methylthio group and the side chain of adenosine appear to play roles in the control of translation. Other thionucleosides like 4-thiouridine and 2-thiocytidine also occur at specific positions in the tRNA molecule. The content of thionucleosides in tRNA from any source varies with the environment. Wide variations in the relative proportions of these modified nucleosides depend on culture conditions, such as growth phase, temperature, degree of aeration and nutritional status. These facts also imply that thionucleosides play important functions in cellular metabolism.

Summary: Naegleria, a genus of amoebae, includes both opportunistically pathogenic and nonpathogenic species. These amoeboflagellates have been isolated from freshwater habitats and soil throughout the world. One species, Naegleria fowleri, is the etiologic agent of primary amoebic meningoencephalitis, a rapidly fatal disease of the central nervous system in humans and experimental animals. The pathogenesis of primary amoebic meningoencephalitis is poorly understood, although highly pathogenic strains of Naegleria spp. show an increased rate of locomotion in response to mammalian cells and increased resistance to complement-mediated lysis. Neither humoral nor cell-mediated immunity appears to play a major role in host defense against infection with N. fowleri. All species of Naegleria are cytopathogenic in vitro, although the mechanisms of cytopathogenesis differ for each species. Cytopathology results from trogocytosis (a specialized type of phagocytosis), cytolytic mechanisms, or a combination of both. The identity of cytotoxic factors produced by these amoebae has not been fully determined. Phospholipases appear to act in concert with other as yet unidentified factors to kill target cells. This review summarizes our current knowledge of the biology of Naegleria spp., including growth, amoeboflagellate transformation, cytopathology in vitro, and host-parasite interactions. Axenic cultivation of these amoebae has made it possible to utilize these organisms to study a number of eucaryotic processes such as gene regulation during transformation from amoeba to flagellate, amoeboid locomotion including chemokinesis and chemotaxis, and mechanisms of target cell destruction.

Summary: The three species of asaccharoyltic black-pigmented Bacteroides, Bacteroides gingivalis, Bacteroides asaccharolyticus, and Bacteroides endodontalis, are typical gram-negative anaerobic rods which are often part of mixed anaerobic infections. However, very little information is known about their specific role in disease. This paper reviews the data concerning the taxonomic problems related to these three species, their ecology and their ultrastructural anatomy, and studies on the pathogenicity of these microorganisms, as well as properties which can affect their virulence potential at least in in vitro models. Finally, we have summarized the data concerning the physiology, serology, and antimicrobial susceptibility of these bacteria. This review should help the reader to understand the relative importance of these three bacterial

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species in infections, to distinguish the specific characters of each species, and to understand some of the microbial factors that may be involved in the initiation and development of disease.

AUTHOR'S CORRECTION

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